

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (canceled)
2. (currently amended) A method for determining whether a beagle dog is an extensive metabolizer or a poor metabolizer in the rate of drug metabolism, said method comprising:
 - preparing a nucleic acid sample from a beagle dog,
 - analyzing a base corresponding to a base at ~~position 1117 of a beagle CYP1A2 gene~~ position 1179 of the nucleotide sequence of SEQ ID NO: 22,
 - determining ~~the~~ a CYP1A2 genotype at the base corresponding to ~~a~~ the base at ~~position 1117 of the beagle CYP1A2 gene~~ position 1179 of the nucleotide sequence of SEQ ID NO: 22, and
 - ~~determining whether~~ judging the beagle dog with a C/C genotype or a C/T genotype to be ~~is an extensive metabolizer and the beagle dog with a T/T genotype to be or a poor metabolizer according to the CYP1A2 genotype.~~
3. (currently amended) A method for selecting a beagle dog used in a medicament test, comprising
 - determining whether a beagle dog is an extensive metabolizer or a poor metabolizer in the rate of drug metabolism by the method according to claim 2, and
 - selecting a beagle dog ~~that is~~ with a C/C genotype or a C/T genotype as the an ~~an~~ extensive metabolizer or a beagle ~~that is~~ dog with a T/T genotype as the a ~~a~~ poor metabolizer.

4. (previously presented) A method for assaying a pharmacological effect and/or toxicity of a test drug, comprising

administering a test drug to an extensive metabolizer group or a poor metabolizer group
selected by the method according to claim 3, and
assaying a pharmacological effect and/or toxicity of the test drug.

5 - 9. (canceled)

10. (currently amended) The method according to ~~claim 9~~claim 3, wherein a beagle dog with the C/C genotype is selected.

11 - 14. (canceled)